SEQUENCE LISTING

<110> Ruelle, Jean-Louis

<120> NEISSERIA MENINGITIDIS ANTIGEN

<130> BM45351

<150> PCT/EP00/00137
<151> 2000-01-10

<160> 6

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Neisseria meningitidis

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cagcgttcgt acaacgcgat tgtcaccgag aaaaacggcg attacagctc gtttgccgtc   180
accgtcggca caaaaatccc cgcttctttg cgcgaaattc cgcaatccgt cagtatcatc   240
accaaccagc aggtcaaaga ccgcaatgtt gatacgtttg accagttggc gcgcaaaacg   300
cccggcctgc gcgtgttgag caacgatgac ggacgctctt cggtttacgc gcgcggttac   360
gaatacagcg aatacaacat cgacggcctg cccgcgcaga tgcagagtat caacggcacg   420
ctgcccaatc tgttcgcctt cgaccgcgtg gaagtgatgc gcgggccgag cggactgttc   480
gacagcagcg gcgagatggg cggtatcgtg aatctggtgc gcaaacgccc gaccaaagcg   540
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gtatcgggca gcctcaattc agacggcagc gtgcgcggcc gcgtgatggc gcagaccgtc   660
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cacgtatttg tcggcgcgga ttggaacaaa tttaaaatga acagccacga cgtgtttgcc   900
gatttgaaac attacttcgg caacggcggc tacggcaaag tcggtatgcg ctattccgac   960
cgcgatgccg actccaacta tgccttttgcc ggcagcaagc tgggcatgaa aaccccggca  1020
ggccgcccgg gctgcaatac ggctgacgac aaagcctgcg cggtgggttt gggtacagaa  1080
atcaaacaaa aagccctcgc gtttgacgcc agctacagca ggcctttccg cttgggcaat  1140
acggccaacg aatttgtcat cggcgccgat tacaaccgct tccgcagcac caacgaacaa  1200
ggccgtacta ctttatatgc acgcggcggc ctggctttaa acgagttccg cagcataccg  1260
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atgcatgcag gcggttatgc cacgttcgat gcgatggcgg cataccgctt cacgcccaag  2040
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<211> 722
<212> PRT
<213> Neisseria meningitidis

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Leu Glu Thr Val His Ile Lys Gly Gln Arg Ser Tyr Asn Ala Ile Val
        35                  40                  45
Thr Glu Lys Asn Gly Asp Tyr Ser Ser Phe Ala Val Thr Val Gly Thr
    50                  55                  60
Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile Ile
65                  70                  75                  80
Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln Leu
                85                  90                  95
Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly Arg
            100                 105                 110
Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile Asp
            115                 120                 125
Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn Leu
    130                 135                 140
Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu Phe
145                 150                 155                 160
Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys Arg
                165                 170                 175
Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr His
            180                 185                 190
Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser Asp
            195                 200                 205
Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser Pro
    210                 215                 220
Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala Ala
225                 230                 235                 240
Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu Tyr
                245                 250                 255
Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala Asn
            260                 265                 270
Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp Trp
            275                 280                 285
Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys His
    290                 295                 300
Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser Asp
305                 310                 315                 320
Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly Met
                325                 330                 335
Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys Ala
            340                 345                 350
Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala Phe
            355                 360                 365
Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn Glu
    370                 375                 380
Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu Gln
385                 390                 395                 400
Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu Phe
                405                 410                 415
Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly Val
            420                 425                 430
Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe Gly
            435                 440                 445
Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu Ile
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          450                      455                      460
Gly Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly Lys
465                      470                      475                      480
Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly Ala
                485                      490                      495
Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser Gln
                500                      505                      510
Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu Lys
                515                      520                      525
Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr Met
        530                      535                      540
Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp Lys
545                      550                      555                      560
Asn Ala Ala Ala Pro Leu Asn Pro Asn Asn Lys Lys Thr Arg Tyr Ala
                565                      570                      575
Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser Gly
            580                      585                      590
Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu His
            595                      600                      605
Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe Leu
        610                      615                      620
Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val Thr
625                      630                      635                      640
Pro Glu Leu Thr Ile Gly Gly Gly Val Asn Ala Met Ser Gly Ile Thr
                645                      650                      655
Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala Met
            660                      665                      670
Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala Asp
        675                      680                      685
Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn Thr
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705                      710                      715                      720
Ser Phe
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<210> 3
<211> 2078
<212> DNA
<213> Neisseria meningitidis

<400> 3

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gcgaaattcc gcaatccgtc agtatcatca ccaaccagca ggtcaaagac cgcaatgttg     180
atacgtttga ccagttggcg cgcaaaacgc ccggcctgcg cgtgttgagc aacgatgacg     240
gacgctcttc ggtttacgcg cgcggttacg aatacagcga atacaacatc gacggcctgc     300
ccgcgcagat gcagagtatc aacggcacgc tgcccaatct gttcgccttc gaccgcgtgg     360
aagtgatgcg cgggccgagc ggactgttcg acagcagcgg cgagatgggc ggtatcgtga     420
atctggtgcg caaacgcccg accaaagcgt tccaaggtca tgctgcggca gggttcggta     480
cgcacaaaca atataaagcc gaggcggacg tatcgggcag cctcaattca gacggcagcg     540
tgcgcggccg cgtgatggcg cagaccgtcg cgcgtctcc gcgtcccgcc gagaaaaaca     600
accggcacga aaccttctac gcggcggcgg attgggacat caaccccgat acggttttgg     660
gcgcgggcta tctttaccag caacgccacc tcgcgccgta caacggcttg ccagccgatg     720
ccaataacaa attaccgtcc ctgccgcaac acgtatttgt cggcgcggat tggaacaaat     780
ttaaaatgaa cagccacgac gtgtttgccg atttgaaaca ttacttcggc aacggcggct     840
acggcaaagt cggtatgcgc tattccgacc gcgatgccga ctccaactat gcctttgccg     900
gcagcaagct gggcatgaaa accccggcag gccgcccggg ctgcaatacg gctgacgaca     960
aagcctgcgc ggtgggtttg ggtacagaaa tcaaacaaaa agccctcgcg tttgacgcca    1020
gctacagcag gcctttccgc ttgggcaata cggccaacga atttgtcatc ggcgccgatt    1080
acaaccgctt ccgcagcacc aacgaacaag ccgtactac tttatatgca cgcggcggcc    1140
tggctttaaa cgagttccgc agcataccgc aggttgattt gattgccaac gcgcgcaaag    1200
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gcgtgcgcgg ttacagccat accgtcgcta ccgaaaacct cgacgaattc ggcatttacg   1260
gcaaatccac cttccatcct gccgacgggc tgtcgcttat cggcggcgga cgtttgggac   1320
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ccggctacgc aggcgcggtt tacgacttga acgacaacaa cagcctctac ctgagcctgt   1440
cccagctcta cacaccgcaa accaacctcg atgccgacgg caagctgctc aaaccgcgcc   1500
aaggcaacca gtttgaagtc ggttacaaag gcagctacat ggacgaccgc ctcaatgccc   1560
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aaaaaacccg ttacgccgca ttgggcaaac gcgtgatgga aggcgttgag accgaaatca   1680
gcggcgcggt tacaccgaaa tggcaaatcc atgcaggtta cagctatctg cacagccaaa   1740
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caaacctgtg gacgacttac caagttacgc ccgagctgac catcggcggc ggagtgaacg   1860
cgatgagcgg cattacttca tctgcaggga tgcatgcagg cggttatgcc acgttcgatg   1920
cgatggcggc ataccgcttc acgcccaagc tgaagctgca aatcaacgcc gacaacatct   1980
tcaaccgcca ttactacgcc cgcgtcggcg gcgcgaacac ctttaacatt cccggttcgg   2040
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<210> 4
<211> 691
<212> PRT
<213> Neisseria meningitidis

<400> 4

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             20                  25                  30
Thr Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile
         35                  40                  45
Ile Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln
     50                  55                  60
Leu Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly
 65                  70                  75                  80
Arg Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile
                 85                  90                  95
Asp Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn
             100                 105                 110
Leu Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu
         115                 120                 125
Phe Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys
     130                 135                 140
Arg Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr
145                 150                 155                 160
His Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser
                 165                 170                 175
Asp Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser
             180                 185                 190
Pro Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala
         195                 200                 205
Ala Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu
     210                 215                 220
Tyr Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala
225                 230                 235                 240
Asn Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp
                 245                 250                 255
Trp Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys
             260                 265                 270
His Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser
         275                 280                 285
Asp Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly
     290                 295                 300
Met Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys
305                 310                 315                 320
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Ala Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala
            325                 330                 335
Phe Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn
            340                 345                 350
Glu Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu
            355                 360                 365
Gln Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu
    370                 375                 380
Phe Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly
385                 390                 395                 400
Val Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe
            405                 410                 415
Gly Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu
            420                 425                 430
Ile Gly Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly
            435                 440                 445
Lys Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly
    450                 455                 460
Ala Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser
465                 470                 475                 480
Gln Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu
            485                 490                 495
Lys Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr
            500                 505                 510
Met Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp
            515                 520                 525
Lys Asn Ala Ala Ala Pro Leu Asn Pro Asn Asn Lys Lys Thr Arg Tyr
    530                 535                 540
Ala Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser
545                 550                 555                 560
Gly Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu
            565                 570                 575
His Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe
            580                 585                 590
Leu Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val
            595                 600                 605
Thr Pro Glu Leu Thr Ile Gly Gly Gly Val Asn Ala Met Ser Gly Ile
    610                 615                 620
Thr Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala
625                 630                 635                 640
Met Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala
            645                 650                 655
Asp Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn
            660                 665                 670
Thr Phe Asn Ile Pro Gly Ser Glu Arg Ser Leu Thr Ala Asn Leu Arg
            675                 680                 685
Tyr Ser Phe
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<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
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<210> 6
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
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